

SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of
Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298

<151> 1999-06-03

<150> 09/701,536

<151> 2000-11-29

<150> 60/087,908

<151> 1998-06-04

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (25) ... (48)

<221> misc_feature

<222> 1-48

<223> Amplimer 14DV389

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48

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<211> 8

<212> PRT

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<223> Description of artificial sequence; note =
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<223> Amplimer c14DV2453

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synthetic construct

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<221> misc_feature
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<210> 5
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<212> PRT
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<223> Description of artificial sequence; note =
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<210> 6
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<222> (25) ... (54)

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<222> 1-54
<223> Amplimer SLEDV410

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51

<210> 8
<211> 9
<212> PRT
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<210> 9
<211> 38
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<213> Artificial Sequence

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<221> misc_feature
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gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu	951
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gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile	1047
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aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	1095
45 50 55 60	
gag aac aga tgc tgg gtc cg ^g gca atc gac gtc ggc tac atg tgt gag Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	1143
65 70 75	
gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	1191
80 85 90	
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	1239
95 100 105	
gga cg ^g tgc acg cg ^g acc agg cat tcc aag cga agc agg aga tcc gtg Gly Arg Cys Thr Arg Thr His Ser Lys Arg Ser Arg Arg Ser Val	1287
110 115 120	
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	1335
125 130 135 140	
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	1383
145 150 155	
tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	1431
160 165 170	
tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu	1479
175 180 185	
ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly	1527
190 195 200	

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gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro 225 230 235	1623
aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu 240 245 250	1671
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val 255 260 265	1719
gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp 270 275 280	1767
agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn 285 290 295 300	1815
gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc Gly Cys Gly Leu Phe Gly Lys Ser Ile Asp Thr Cys Ala Lys Phe 305 310 315	1863
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile 320 325 330	1911
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn 335 340 345	1959
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360	2007
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr 365 370 375 380	2055
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu 385 390 395	2103
gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg 400 405 410	2151
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca	2199

Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr		
415	420	425
gct tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gct cac gcc		2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala		
430	435	440
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat		2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His		
445	450	455
cag gct ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag		2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys		
465	470	475
tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct		2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala		
480	485	490
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg		2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala		
495	500	505
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc		2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser		
510	515	520
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg		2535
Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala		
525	530	535
540		
agc ctc aat gac atg acc ccc gtt ggg cggt gtg aca gtg aac ccc		2583
Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro		
545	550	555
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa		2631
Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu		
560	565	570
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag		2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln		
575	580	585
atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt		2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe		
590	595	600
tca aca act ttg aag gga gct caa aga ctg gca gct ttg ggc gac aca		2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr		
605	610	615
620		
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa		2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys		
625	630	635

gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga	2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly	
640	645
650	
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg	2919
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met	
655	660
665	
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca	2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr	
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Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala *	
685	690
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aagcatttat	cagg	tttgc	tttgc	tttca	tttca	7449	
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<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<223> pCDJE 2-7

<400> 11
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20 25 30
Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
35 40 45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
50 55 60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65 70 75 80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85 90 95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100 105 110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
115 120 125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
130 135 140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145 150 155 160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165 170 175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val
180 185 190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210 215 220
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225 230 235 240
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
245 250 255
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
260 265 270
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
275 280 285
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
290 295 300
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305 310 315 320
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325 330 335
Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr
340 345 350
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
355 360 365
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
370 375 380
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385 390 395 400
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
 420 425 430
 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
 435 440 445
 Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
 450 455 460
 Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
 465 470 475 480
 His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
 485 490 495
 Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
 500 505 510
 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
 515 520 525
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
 530 535 540
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
 545 550 555 560
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
 565 570 575
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
 580 585 590
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
 595 600 605
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
 610 615 620
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
 625 630 635 640
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
 645 650 655
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
 660 665 670
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
 675 680 685
 Val Phe Leu Ala Thr Asn Val His Ala
 690 695

<210> 12
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature
 <222> 1-46
 <223> WN 466

<400> 12
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<210> 13
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-43
<223> CWN2444

<400> 13
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<210> 14
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<223> JE Signal

<400> 14
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Cys Ala Gly Ala
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<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (911) ... (2987)

<221> misc_feature
<222> (1) ... (5308)
<223> pCBWN

<400> 15
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ccgcatagtt aagccagtat ctgctccctg ctttgtgttt ggagggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggtag gcgtttgcg ctgttcgcg atgtacgggc cagatatacg cggttgcatt	240
gattattgac tagttattaa tagtaatcaa ttacgggtc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgc tggctgaccg cccaaacgacc	360
cccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
attgacgtca atgggtggag tatttacgt aaactgccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgaccta tgggacttc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggttttgg cagtagatca atggcgtgg atagcggtt	660
gactcacggg gatccaag tctccacccc attgacgtca atggagatggtt gtttggcac	720
caaaatcaac gggactttcc aaaatgtcgt aacaactccg ccccatgtac gcaaattggc	780
ggtaggcgtg tacggtgga ggtctatata agcagagctc tctggcta ac tagagaaccc	840
actgcttact ggcttatcga aattaatacg actcaactata gggagaccca agcttggtac	900
cggccgcgcg atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg	949
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala	
1 5 10	
agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac	997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn	
15 20 25	
ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat	1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp	
30 35 40 45	
gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga	1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg	
50 55 60	
gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys	
65 70 75	
cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc	1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys	
80 85 90	
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
95 100 105	
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	
agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc	1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
130 135 140	
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga	1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly	
145 150 155	

tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr 160 165 170	1429
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct Met Gln Arg Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala 175 180 185	1477
tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly 190 195 200 205	1525
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys 210 215 220	1573
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met 225 230 235	1621
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu 240 245 250	1669
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly 255 260 265	1717
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln 270 275 280 285	1765
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys 290 295 300	1813
gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile 305 310 315	1861
gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe 320 325 330	1909
gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln 335 340 345	1957
gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro 350 355 360 365	2005
tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt	2053

Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys			
370	375	380	
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt			2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val			
385	390	395	
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac			2149
Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn			
400	405	410	
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg			2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr			
415	420	425	
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca			2245
Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala			
430	435	440	445
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att			2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile			
450	455	460	
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg			2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu			
465	470	475	
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat			2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr			
480	485	490	
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca			2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr			
495	500	505	
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga			2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly			
510	515	520	525
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg			2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr			
530	535	540	
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg			2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr			
545	550	555	
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca			2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser			
560	565	570	
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac			2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His			
575	580	585	

aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly 590 595 600 605	2725
gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca Ala Gln Arg Leu Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser 610 615 620	2773
gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe 625 630 635	2821
gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln 640 645 650	2869
gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp 655 660 665	2917
agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe 670 675 680 685	2965
ctc tcc gtg aac gtg cac gcc t gaaggcgcc gctcgagcat gcattctagag Leu Ser Val Asn Val His Ala 690	3017
ggccctattc tatagtgtca cctaaatgct agagctcgct gatcaggcctc gactgtgcct tctagttgcc agccatctgt tggttgcccc tcccccggtc cttccttgac cctggaaagg gcacactccca ctgtccttcc ctaataaaaat gaggaaattg catcgatttgc tctgagtagg tgtcattcta ttctgggggg tgggggtgggg caggacagca agggggagga ttgggaagac aatagcagggc atgctggggta tgcgggtgggc tctatggctt ctgaggcgga aagaaccagc tgcattatgc aatcgccaa cgccggggga gagggcggtt gctgtattttggg cgctcttcc cttcctcgct cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gatatcgctc actcaaaggc ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaaggc ccagcaaaag gccaggaacc gtaaaaaggc cgctgttgcg gctttttcc ataggctccg ccccccgtac gagcatcaca aaaatcgacg ctcaagtctc aggtggcgaa acccgacagg actataaaga taccaggcg ttcggccctgg aagctccctc gtgcgtctc ctgttccgac cctgcgtt accggatacc tgcgttgc tctcccttcg ggaagcgtgg cgctttctca tagctcacgc tgcgttgc tgcgttgc gtaggtcggt cgctccaagc tgggtgtgt gcacgaaacc cccgttcagc ccgaccgctg cgccattatcc ggttaactatc gtcttgagtc caaccggta agacacgact tatacgccact ggcagcagcc actggtaaca ggatttagcaag agcgaggtat gtggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac tagaagaaca gtatggta tctgcgtt gctgaagcca gttaccttcg gaaaaagagt tggtagctt tgatccggca aacaaaccac cgctggtagc ggtggtttt ttgtttgcaa gcagcagatt acgcccggaa aaaaaggatc tcaagaagat cctttgatct tttctacgg gtctgacgct cagtgaaacg aaaactcacg ttaaggatt ttggcatga gattatcaaa aaggatctt acctagatcc tttaaaatcaaaaatgaatgt tttaaatcaa tctaaagtat atatgagtaa acttggcttg acagttacca atgcttaatc agtgaggcac ctatctcaggc gatctgtcta ttccgttcat ccatacgatgc ctgactcccc gtcgtttaga taactacgat acgggaggccc ttaccatctg gcccactgc tgcaatgata cccgcgagacc cacgctcacc ggctccagat ttatcagcaaa taaaaccagcc agccggaaagg gcccggcc	3077 3137 3197 3257 3317 3377 3437 3497 3557 3617 3677 3737 3797 3857 3917 3977 4037 4097 4157 4217 4277 4337 4397 4457 4517

gaagtggtcc tgcaacttta tccgcctcca tccagtcata taattgttgc cggaaagcta	4577
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tgggtcactc ctcgtcgaaa ggtatggctt cattcagctc cggttcccaa cgatcaaggc	4697
gagttacatg atccccatg ttgtcaaaa aagcggttag ctccctcggt cctccgatcg	4757
ttgtcagaag taagttggcc gcagtgttat cactcatggt tatggcagca ctgcataatt	4817
ctcttactgt catgcacatcc gtaagatgct tttctgtgac tggtagtac tcaaccaagt	4877
cattctgaga atagtgtatg cgccgaccga gttgctcttg cccggcgtca atacggata	4937
ataccgcgcc acatagcaga actttaaaag tgctcatcat tggaaaacgt tcttcggggc	4997
gaaaactctc aaggatctt ccgctgttga gatccagttc gatgtAACCC actcgtgcac	5057
ccaaactgatc ttccagcatct ttactttca ccagcgtttc tgggtgagca aaaacaggaa	5117
ggcaaaatgc cgcaaaaaag ggaataaggg cgacacggaa atgttgaata ctcatactct	5177
tccttttca atattattga agcatttatac agggttatttgc tctcatgagc ggatacatat	5237
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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBWN

<400> 16

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Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Val	Thr	Leu	Ser	Asn	Phe	Gln	Gly
									20			25			30
Lys	Val	Met	Met	Thr	Val	Asn	Ala	Thr	Asp	Val	Thr	Asp	Val	Ile	Thr
									35			40			45
Ile	Pro	Thr	Ala	Ala	Gly	Lys	Asn	Leu	Cys	Ile	Val	Arg	Ala	Met	Asp
									50			55			60
Val	Gly	Tyr	Met	Cys	Asp	Asp	Thr	Ile	Thr	Tyr	Glu	Cys	Pro	Val	Leu
									65			70			75
Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Thr	Lys	Ser
									85			90			95
Ala	Val	Tyr	Val	Arg	Tyr	Gly	Arg	Cys	Thr	Lys	Thr	Arg	His	Ser	Arg
									100			105			110
Arg	Ser	Arg	Arg	Ser	Leu	Thr	Val	Gln	Thr	His	Gly	Glu	Ser	Thr	Leu
									115			120			125
Ala	Asn	Lys	Lys	Gly	Ala	Trp	Met	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr
									130			135			140
Leu	Val	Lys	Thr	Glu	Ser	Trp	Ile	Leu	Arg	Asn	Pro	Gly	Tyr	Ala	Leu
									145			150			155
Val	Ala	Ala	Val	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Thr	Met	Gln	Arg
									165			170			175
Val	Val	Phe	Val	Val	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	
									180			185			190
Asn	Cys	Leu	Gly	Met	Ser	Asn	Arg	Asp	Phe	Leu	Glu	Gly	Val	Ser	Gly
									195			200			205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
 210 215 220
 Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
 225 230 235 240
 Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
 245 250 255
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
 260 265 270
 Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
 275 280 285
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300
 Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
 305 310 315 320
 Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335
 Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
 340 345 350
 Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
 355 360 365
 Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
 370 375 380
 Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
 385 390 395 400
 Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
 405 410 415
 Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
 420 425 430
 Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
 435 440 445
 Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
 450 455 460
 Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
 465 470 475 480
 Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
 485 490 495
 Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
 500 505 510
 Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
 515 520 525
 Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
 530 535 540
 Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
 545 550 555 560
 Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
 565 570 575
 Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
 580 585 590
 Ser Ser Ile Gly Lys Ala Phe Thr Thr Leu Lys Gly Ala Gln Arg
 595 600 605
 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
 610 615 620
 Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
 625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
 645 650 655
 Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
 660 665 670
 Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
 675 680 685
 Asn Val His Ala
 690

<210> 17
<211> 5334
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (916) ... (3007)
<221> misc_feature
<222> (1)...(5334)
<223> pCBJE 1-14

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180
tttagggtag gcgtttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggag tatttacggt aaactgccc cttggcagta catcaagtgt 480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaaatggccc gcctggcatt 540
atgcccagta catgaccccta tgggactttc ctacttggca gtacatctac gtattagtca 600
tcgctattac catggtgatg cgggtttggc agtacatcaa tgggcgtgga tagcggtttg 660
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ctgcttactg gcttatcgaa attaatacg ctcactatag ggagacccaa gcttggtacc 900
tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa 951
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
 1 5 10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg 999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
 15 20 25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc 1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
 30 35 40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly 45 50 55 60	1095
gag aac aga tgc tgg gtc cg ^g gca atc gac gtc ggc tac atg tgt gag Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu 65 70 75	1143
gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro 80 85 90	1191
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr 95 100 105	1239
gga cg ^g tgc acg cg ^g acc agg cat tcc aag cga agc agg aga tcc gtg Gly Arg Cys Thr Arg Thr His Ser Lys Arg Ser Arg Arg Ser Val 110 115 120	1287
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala 125 130 135 140	1335
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn 145 150 155	1383
tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly 160 165 170	1431
tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu 175 180 185	1479
ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly 190 195 200	1527
aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu 205 210 215 220	1575
gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro 225 230 235	1623
aca ttg gac gtc cg ^g atg att aac atc gaa gct agc caa ctt gct gag Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu 240 245 250	1671
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg	1719

Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val			
255	260	265	
gct cggtgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat			1767
Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp			
270	275	280	
agt agc tat gtgtgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac			1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn			
285	290	295	300
ggttgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc			1863
Gly Cys Gly Leu Phe Gly Lys Ser Ile Asp Thr Cys Ala Lys Phe			
305	310	315	
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc			1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile			
320	325	330	
aaa tac gaa gtt ggc att ttt gtgtcat gga acc acc act tcg gaa aac			1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn			
335	340	345	
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt			2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe			
350	355	360	
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac			2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr			
365	370	375	380
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa			2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu			
385	390	395	
gcgttt tac gtc atg acc gtgg tca aag tca ttt ctg gtc cat agg			2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg			
400	405	410	
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca			2199
Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr			
415	420	425	
gcgtgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc			2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala			
430	435	440	
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat			2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His			
445	450	455	460
cag gcgttg gca gga gcc atc gtgtgtg gag tac tca agc tca gtg aag			2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys			
465	470	475	

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala 480 485 490	2391
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495 500 505	2439
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510 515 520	2487
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525 530 535 540	2535
agc ctc aat gac atg acc ccc gtt ggg cg ^g ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545 550 555	2583
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu 560 565 570	2631
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln 575 580 585	2679
atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe 590 595 600	2727
tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr 605 610 615 620	2775
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635	2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650	2871
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met 655 660 665	2919
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr 670 675 680	2967
ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct t aatttagttg	3017

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
 685 690 695

agcggccgct	cgagcatgca	tctagagggc	cctattctat	agtgtcacct	aaatgctaga	3077	
gctcgctgat	cagcctcgac	tgtgccttct	agtgcgcagc	catctgttgt	ttgcccctcc	3137	
cccggtcct	ccttgaccct	ggaagggtgcc	actcccactg	tcctttccta	ataaaaatgag	3197	
gaaattgcat	cgcattgtct	gagtaggtgt	cattctattc	tgggggggtgg	ggtggggcag	3257	
gacagcaagg	gggaggattg	ggaagacaat	agcaggcatg	ctggggatgc	ggtgggctct	3317	
atggcttctg	aggcgaaag	aaccagctgc	attaatgaat	cggccaaacgc	gccccggagag	3377	
gcggttgcg	tattggcgc	tcttccgctt	cctcgctcac	tgactcgctg	cgctcggtcg	3437	
ttcggctcg	gcgagcggt	tcagctca	caaaggcggt	aatacgttta	tccacagaat	3497	
caggggataa	cgcaggaaag	aacatgtgag	caaaaggcca	gaaaaaggcc	aggaaccgta	3557	
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cggccactggc	agcagccact	ggtAACAGGA	ttagcagagc	gaggatgt	ggcgggtgcta	3977	
cagagttctt	gaagtgg	cctaactac	gctacactag	aagaacagta	tttgttatct	4037	
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aaaccaccgc	ttgttagcggt	ggttttttt	tttgcagca	gcagattacg	cgccggaaaa	4157	
aaggatctca	agaagatcct	ttgatcttt	ctacgggtc	tgacgctc	tgaacgaaa	4217	
actcacgtt	agggatttt	gtcatgagat	tatcaaaaag	gatcttacc	tagatcctt	4277	
taaattaaaa	atgaagttt	aatcaatct	aaagtatata	tgagtaaact	tttgtctgaca	4337	
gttaccaat	cttaatcagt	gaggcacca	tctcagcgat	ctgtctattt	cgttcatcca	4397	
tagttgc	actccccgtc	gtgtagataa	ctacgatac	ggagggctt	ccatctggcc	4457	
ccagtgcgtc	aatgatacc	cgagaccac	gctaccggc	tccagattt	tcagcaataa	4517	
accagccagc	cggaagg	gagcgcagaa	gtggcctgc	aactttatcc	gcctccatcc	4577	
agtctat	ttgttgc	gaaagctag	taagtagttc	gccagttat	agtttgcgc	4637	
acgttgttgc	cattgtaca	ggcatcg	tgtcacgtc	gtcggttgg	atggcttcat	4697	
tca	ccgttccgg	ttcccaac	tcaaggcag	ttacatgatc	ccccatgtt	tgcaaaaaag	4757
cggttagctc	cttcgg	ccgatcg	tcagaagtaa	gttggccgca	gtgttatcac	4817	
tcatggttat	ggcagact	cataattctc	ttactgtcat	gccatccgta	agatgtttt	4877	
ctgtgactgg	tgagtact	accaggat	tctgagaata	gtgtatcg	cgaccgagtt	4937	
gctcttgc	ggcgtcaata	cgggataata	ccgcgcaca	tagcagaact	ttaaaaagtgc	4997	
tcatcattgg	aaaacgttct	tcggggcgaa	aactctcaag	gatcttacc	ctgttgagat	5057	
ccagttcgat	gtAACCCACT	cgtgcaccca	actgatctc	agcatcttt	atttcacca	5117	
gcgttctgg	gtgagcaaaa	acaggaaaggc	aaaatggc	aaaaaaggga	ataaggcga	5177	
cacggaaatg	ttgaataact	atactcttcc	ttttcaata	ttattgaagc	atttatcagg	5237	
gttattgtct	catgagcg	tacatattt	aatgtattt	aaaaataaaa	caaataagggg	5297	
ttccgcgcac	atttcccc	aaagtccac	ctgacgt			5334	

<210> 18
 <211> 697
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<223> pCBJE 1-14

<400> 18
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Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30
Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
35 40 45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
50 55 60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65 70 75 80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85 90 95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100 105 110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
115 120 125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
130 135 140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145 150 155 160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165 170 175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
180 185 190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210 215 220
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225 230 235 240
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
245 250 255
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
260 265 270
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
275 280 285
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
290 295 300
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305 310 315 320
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325 330 335
Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr
340 345 350
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
355 360 365
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
370 375 380
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385 390 395 400
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
 420 425 430
 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
 435 440 445
 Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
 450 455 460
 Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
 465 470 475 480
 His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
 485 490 495
 Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
 500 505 510
 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
 515 520 525
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
 530 535 540
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
 545 550 555 560
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
 565 570 575
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
 580 585 590
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
 595 600 605
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
 610 615 620
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
 625 630 635 640
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
 645 650 655
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
 660 665 670
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
 675 680 685
 Val Phe Leu Ala Thr Asn Val His Ala
 690 695

<210> 19
 <211> 5283
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> CDS
 <222> (910) ... (2965)

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 ccgcatagtt aagccagtat ctgctccctg ctttgtgttt ggagggtcgct gagtagtgcg 120
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180
 tttagggtag gcgtttcgct ctgcttcgct atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacgggtc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccAACGACC	360
cccgcccatt gacgtcaata atgacgtatg ttccatagt aacgcataa gggactttcc	420
attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgacccta tggacttcc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggtttggc agtacatcaa tggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttggcacc	720
aaaatcaacg ggacttcca aaatgtcgta acaactccgc cccattgacg caaatggcgg	780
gtaggcgtgt acggtggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc	900
gccgcccgcgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
 ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac	999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp	
15 20 25 30	
 agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc	1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser	
35 40 45	
 cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg	1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met	
50 55 60	
 gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac	1143
Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp	
65 70 75	
 cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat	1191
Gln Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp	
80 85 90	
 agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg	1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg	
95 100 105 110	
 ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc	1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val	
115 120 125	
 ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc	1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val	
130 135 140	
 acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc	1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala	
145 150 155	
 att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg	1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val	
160 165 170	

act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg		1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg		
175	180	185
		190
tgc acg cat ctt gag aac aga gat ttt gtg aca gga actcaa ggg acc		1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr		
195	200	205
acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca		1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr		
210	215	220
gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag		1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln		
225	230	235
gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc		1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr		
240	245	250
aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt		1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu		
255	260	265
270		
ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac		1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp		
275	280	285
cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg		1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val		
290	295	300
gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac		1863
Ala Cys Ala Lys Phe Glu Cys Glu Ala Lys Lys Ala Val Gly His		
305	310	315
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac		1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His		
320	325	330
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca		1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser		
335	340	345
350		
gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac		2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp		
355	360	365
tat gga gat gtg tcg acg tgt aaa gtg gca agt ggg att gat gtc		2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val		
370	375	380
gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct		2103

Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro		
385	390	395
tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc		2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro		
400	405	410
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg		2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val		
415	420	425
gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg		2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly		
435	440	445
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc		2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala		
450	455	460
agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt		2343
Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys		
465	470	475
gat gtg gga ctg gaa aag ctg aaa ggc aca acc tac tcc atg		2391
Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met		
480	485	490
tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc		2439
Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly		
495	500	505
cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca		2487
His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro		
515	520	525
tgt cgg atc ccc gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat		2535
Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn		
530	535	540
gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc		2583
Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly		
545	550	555
gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg		2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val		
560	565	570
gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga		2679
Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg		
575	580	585
atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga		2727
Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly		
595	600	605

gaa cat gca tgg gac ttt ggc tca gta ggc ggg gta ctg tct tct gtg	2775
Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val	
610	615
620	
ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt	2823
Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe	
625	630
635	
ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc	2871
Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val	
640	645
650	
tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt	2919
Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu	
655	660
665	670
gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca t	2965
Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala	
675	680
685	
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ggaaattgca tcgcattgtc tgagttaggtg tcattctatt ctgggggtg ggttggggca	3205
ggacagcaag ggggaggatt gggaaagacaa tagcaggcat gctggggatg cggtgggctc	3265
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accgctgcgc ttatccggta aactatcgta ttgagtccaa cccggtaaga cacgacttat	3865
cggcaactggc agcagccact ggtAACAGGA ttagcagagc gaggtatgta ggcggtgcta	3925
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gcgtttctgg	gtgagcaaaa	acaggaaggc	aaaatgccgc	aaaaaaaggga	ataagggcga	5125
cacggaaatg	ttgaatactc	atactcttcc	ttttcaata	ttattgaagc	atttatcagg	5185
gttattgtct	catgagcgg	tacatatttgc	aatgtattta	gaaaaataaa	caaatagggg	5245
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<210> 20

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 20

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Trp	Leu	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Phe	Ser
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Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp
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Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu
	65				70				75						80
Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
					85				90						95
Val	Ala	Tyr	Gly	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg	
					100			105			110				
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
							115		120				125		
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys
						130		135				140			
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu
	145				150				155						160
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
						165			170						175
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile
						180			185						190
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
						195		200				205			
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
						210		215			220				
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
	225				230				235						240
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
						245			250						255
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
						260			265						270
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
						275		280			285				

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
 290 295 300
 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
 305 310 315 320
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
 325 330 335
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
 340 345 350
 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
 355 360 365
 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
 370 375 380
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
 385 390 395 400
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
 405 410 415
 His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
 420 425 430
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
 435 440 445
 Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Leu Tyr Lys Leu
 450 455 460
 His Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
 465 470 475 480
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
 500 505 510
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
 565 570 575
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
 610 615 620
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
 625 630 635 640
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
 645 650 655
 Arg Asn Met Thr Met Ser Met Ser Ile Leu Val Gly Val Ile Met
 660 665 670
 Met Phe Leu Ser Leu Gly Val Gly Ala
 675 680

<210> 21
 <211> 5304
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910) ... (2986)

<400> 21

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc	180
ttagggtttag gcgttttcgc ctgcttcgcg atgtacgggc cagatatacg cgttgacatt	240
gattattgac tagttattaa tagtaatcaa ttacgggttc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc	360
cccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
atgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgaccta tgggactttc ctacttggca gtacatctac gtattagtca	600
tcgcttattac catggtgatg cgggtttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttgc acc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccatggacg caaatggcgc	780
gtaggcgtgt acgggtggag gtctatataa gcagagctct ctggctact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc	900
gccggccccc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser

1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat	999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr	
15 20 25 30	

cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc	1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala	
35 40 45	

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct	1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala	
50 55 60	

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca	1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro	
65 70 75	

gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac	1191
Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp	
80 85 90	

gtc gaa gag gtg tgg gtg cac tac ggc aga tgc acg cgc atg gga cat	1239
Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His	
95 100 105 110	

tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc	1287
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Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser
 115 120 125
 aca ctg gca aca aag aac acg cca tgg ttg gac acc gtc aaa acc acc acc 1335
 Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr
 130 135 140
 aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat 1383
 Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr
 145 150 155
 gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca 1431
 Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr
 160 165 170
 cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac 1479
 Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr
 175 180 185 190
 agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc 1527
 Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala
 195 200 205
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 Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val
 210 215 220
 aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag 1623
 Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys
 225 230 235
 atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca 1671
 Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala
 240 245 250
 acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa 1719
 Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu
 255 260 265 270
 gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat 1767
 Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp
 275 280 285
 gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg 1815
 Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
 290 295 300
 agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg 1863
 Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly
 305 310 315
 aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg 1911
 Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val
 320 325 330

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gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys 385 390 395	2103
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu 400 405 410	2151
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu 415 420 425 430	2199
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta Val Glu Phe Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu 435 440 445	2247
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro 450 455 460	2295
gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa Ala Thr Val Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys 465 470 475	2343
tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly 480 485 490	2391
atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly 495 500 505 510	2439
cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro 515 520 525	2487
tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro 530 535 540	2535
gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg	2583

Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala			
545	550	555	
aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac			2631
Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr			
560	565	570	
atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa			2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys			
575	580	585	590
gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc			2727
Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala			
595	600	605	
caa cggttta gtc tta ggg gac aca gcg tgg gac ttt gga tct att			2775
Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile			
610	615	620	
gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga			2823
Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly			
625	630	635	
gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg			2871
Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly			
640	645	650	
cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg			2919
Leu Leu Gly Ala Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg			
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agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg			2967
Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu			
675	680	685	
gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg			3016
Ala Thr Ser Val Gln Ala			
690			
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<210> 22
<211> 692
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 22
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
20 25 30
Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
35 40 45
Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
50 55 60
Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65 70 75 80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
85 90 95
Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100 105 110
Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115 120 125
Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
 145 150 155 160
 Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
 165 170 175
 Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
 180 185 190
 Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
 195 200 205
 Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Ser Cys Val Thr Val
 210 215 220
 Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
 225 230 235 240
 Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
 245 250 255
 Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
 260 265 270
 Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
 275 280 285
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300
 Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
 305 310 315 320
 Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335
 Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
 340 345 350
 Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
 355 360 365
 Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
 370 375 380
 Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
 385 390 395 400
 Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
 405 410 415
 Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
 420 425 430
 Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
 435 440 445
 Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
 450 455 460
 Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
 465 470 475 480
 Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
 485 490 495
 Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
 500 505 510
 Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
 515 520 525
 Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
 530 535 540
 Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
 545 550 555 560
 Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
 565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
 580 585 590
 Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
 595 600 605
 Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
 610 615 620
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
 625 630 635 640
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
 645 650 655
 Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
 660 665 670
 Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
 675 680 685
 Ser Val Gln Ala
 690

<210> 23
<211> 5271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (910)...(2953)

<400> 23
gacggatcgg gagatctccc gatccccat ggtcgactct cagtaatac tgctctgatg 60
ccgcatatgtt aagccagtat ctgctccctg cttgtgtgtt ggaggcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180
ttagggttag gcgtttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagtattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt 480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgcccagta catgaccta tggacttcc ctacttggca gtacatctac gtattagtca 600
tcgctattac catggtgatg cgggtttggc agtacatcaa tggcggttgc tagcggtttg 660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tggagtttgc ttttggcacc 720
aaaatcaacg ggacttcca aaatgtcgta acaactccgc cccattgacg caaatggcg 780
gtagggcgtgt acgggtggag gtctatataa gcagagctct ctggcttaact agagaaccca 840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gtttggtacc 900
gccggccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
 15 20 25 30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047

Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr				
35	40	45		
ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag				1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys				
50	55	60		
tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca				1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro				
65	70	75		
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac				1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn				
80	85	90		
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg				1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg				
95	100	105	110	
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag				1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys				
115	120	125		
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc				1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu				
130	135	140		
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg				1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr				
145	150	155		
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc				1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val				
160	165	170		
gtg att gcc cta ctg gtc ttg gct ggt ccg gcc tac tca gct cac				1479
Val Ile Ala Leu Leu Val Ala Val Gly Pro Ala Tyr Ser Ala His				
175	180	185	190	
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga				1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly				
195	200	205		
act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg				1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met				
210	215	220		
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att				1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile				
225	230	235		
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act				1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr				
240	245	250		

cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu 255 260 265 270	1719
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp 275 280 285	1767
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val 290 295 300	1815
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val 305 310 315	1863
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly 320 325 330	1911
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat Ala Lys Gln Glu Asn Trp Thr Asp Ile Lys Thr Leu Lys Phe Asp 335 340 345 350	1959
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala 355 360 365	2007
aca ctg gaa tgc cag gtgcaa act gcg gtg gac ttt ggt aac agt tac Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr 370 375 380	2055
atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc Ile Ala Glu Met Glu Ser Trp Ile Val Asp Arg Gln Trp Ala 385 390 395	2103
cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Val Trp Arg 400 405 410	2151
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile 415 420 425 430	2199
aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu 435 440 445	2247
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr 450 455 460	2295
aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg	2343

Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu		
465	470	475
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt		2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe		
480	485	490
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg		2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val		
495	500	505
aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat		2487
Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp		
515	520	525
gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc		2535
Asp Leu Thr Ala Ala Asn Lys Gly Ile Leu Val Thr Val Asn Pro		
530	535	540
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct		2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro		
545	550	555
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act		2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr		
560	565	570
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag		2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln		
575	580	585
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg		2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp		
595	600	605
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att		2775
Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile		
610	615	620
cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac		2823
His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn		
625	630	635
tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc		2871
Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile		
640	645	650
aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg		2919
Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val		
655	660	665
atc atg atg ttt ttg tct cta gga gtt ggg gcg t gagcggccgc		2963
Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala		
675	680	

tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaaatgctag agctcgctga 3023
 tcagcctcga ctgtgccttc tagttgccag ccacatgttg tttgccctc cccccgtgcct 3083
 tccttgacct tggaaagggtc cactcccact gtccttctt aataaaaatga ggaaattgca 3143
 tcgcattgtc tgtagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag 3203
 ggggaggatt gggaaagacaa tagcaggcat gctggggatg cgggtggctc tatggcttct 3263
 gaggcgaaaaa gaacagctgc attaatgaat cgcccaacgc gcggggagag gcgggttgcg 3323
 tattggcgcc tcttcgcctt cctcgctcac tgactcgctg cgctcgctg ttccggctgcg 3383
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 gttgctggcg tttttccata ggctccgccc ccctgacgag catcacaat atcgacgctc 3563
 aagtcaaggg tggcgaaacc cgacaggact ataaagatac caggcggttc cccctggaaag 3623
 ctcccctcggt cgcttcgcctt ttccgacccct gccgcttacc ggataacctgt ccgcctttct 3683
 cccttcggga agcgtggcgc tttctcaatg ctcacgtgt aggtatctca gttcggtgt 3743
 ggtcggtcgc tccaaagctgg gctgtgtca cgaacccccc gttcagcccg accgctgcgc 3803
 cttatccggta aactatcgtc ttgagtc当地 cccggtaaga cacgacttat cgccactggc 3863
 agcagccact ggtaaacagga ttagcagagc gaggtatgtt ggcgggtgcta cagagttctt 3923
 gaagtgggtgg cctaaactacg gctacactag aaggacagta tttggtatct ggcgtctgct 3983
 gaagccagtt accttcggaa aaagagtgg tagctcttga tccggcaaaac aaaccaccgc 4043
 tggtagcggt ggttttttgg tttcaagca gcagattacg cgccggaaaaa aaggatctca 4103
 agaagatccct ttgatctttt ctacggggcgc tgacgctcag tggaaacgaaa actcacgtta 4163
 agggatttttgg gtcatgagat tatcaaaaag gatcttcacc tagatcctt taaaattaaaa 4223
 atgaagttttt aaatcaatct aaagtatata tgagtaaact tggctctgaca gtacccaatg 4283
 cttaatcagt gaggcaccta tctcagcgtat ctgtcttattt cgttcatcca tagttgcctg 4343
 actccccgtc gtgtagataa ctacgatacg ggagggttta ccatctggcc ccagtgcgtc 4403
 aatgataccg cgagacccac gctcaccggc tccagattta tcagcaataa accagccagc 4463
 cggaaaggccg gggcgccagaa gtggctctgc aactttatcc gcctccatcc agtctattaa 4523
 ttgttgcggg gaagctagag taagtagttc gccagttat agtttgcgc acgttgggtc 4583
 cattgctaca ggcacatcggtt gtcacgctc gtgtttggat atggcttcat tcaagctccgg 4643
 ttcccaacga tcaaggcgag ttacatgatc cccatgttg tgcaaaaaag cggttagctc 4703
 ctccggcctt ccgatcggtt tcagaagataa gttggccgcgtt gtttatcactcatgtt 4763
 ggcagcactg cataattctc ttactgtcat gccatccgtt agatgtttt ctgtgactgg 4823
 tgtagtactca accaagtcat tctgagaata gtgtatgcgg cgaccgagtt gcttttgcctt 4883
 ggcgtcaata cgggataata ccggccaca tagcagaact taaaatgtc tcatcattgg 4943
 aaaaacgttct tcggggcgaa aactctcaag gatcttaccg ctgtttagat ccagttcgat 5003
 gtaacccact cgtgcaccca actgatcttc agcatctttt actttcacca gcttttctgg 5063
 gtgagcaaaa acaggaaggc aaaatgcccgc aaaaaaggga ataaggcga cacggaaatg 5123
 ttgaataactc atactttcc ttttcaata ttattgaagc atttatcagg gtattgtct 5183
 catgagcgga tacatatttgg aatgttattta gaaaaataaaa caaataagggg ttccgcgcac 5243
 atttccccgaa aaagtgcac ctgacgtc 5271

<210> 24
 <211> 681
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<400> 24
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
20 25 30
Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
35 40 45
Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
50 55 60
Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65 70 75 80
Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
85 90 95
Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
100 105 110
Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
115 120 125
Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
130 135 140
Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145 150 155 160
Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
165 170 175
Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
180 185 190
Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
195 200 205
Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
210 215 220
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225 230 235 240
Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
245 250 255
Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
260 265 270
Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
275 280 285
Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300
Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305 310 315 320
Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
325 330 335
Gln Glu Asn Trp Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
340 345 350
Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
355 360 365
Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
370 375 380
Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
385 390 395 400
Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
405 410 415
His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
420 425 430
Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
 450 455 460
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
 465 470 475 480
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
 500 505 510
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
 565 570 575
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
 610 615 620
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
 625 630 635 640
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
 645 650 655
 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
 660 665 670
 Met Phe Leu Ser Leu Gly Val Gly Ala
 675 680

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-35

<223> POW 454

<400> 25

aaaagaaaaaa gcgctaccac catccaccgg gacag

35

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> CPOW 2417

<400> 26
actgttaccc tcaaccccg actcgccggc gaaaaagaaa a 41

<210> 27
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<223> Modified JE Signal

<400> 27
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Gly Thr Ser Ala
20

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-36
<223> YF 482

<400> 28
aaaaagaaaaaa gcgctgtgac cttggcggg aaaaac 36

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> CYF 2433

<400> 29
acagagatcc tcaaccccgcc actcgccggc gaaaaagaaaa a

41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> SLE 463

<400> 30
aaaagaaaaaa gcgcgttgca gttatcaacc tatcaggggaa a

41

<210> 31
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-40
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaaagaaaa

40